U.S. Serial No.: 10/659,055
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AMENDMENTS TO THE CLAIMS

The following listing of claims replaces all prior versions, and listings, of claims in this application.

Listing of Claims

1. (Currently amended) A composition comprising a protein in crystalline form, wherein the protein consists of ~~SEQ. ID No. 3~~ SEQ ID NO:3, and wherein the protein crystal has a crystal lattice in a $P2_1$ space group and unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å, $\alpha=\gamma=90°$, $\beta=114.6°$.

2-3. (Cancelled)

4. (Previously presented) A composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution less than 3.0 Angstroms.

5-6. (Canceled)

7. (Currently amended) A method for forming a crystal of a protein comprising:
    forming a crystallization volume comprising a precipitant solution and a protein that consists of ~~SEQ. ID No. 3~~ SEQ ID NO:3, and wherein the protein crystal has a crystal lattice in a $P2_1$ space group and unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å, $\alpha=\gamma=90°$, $\beta=114.6°$; and
    storing the crystallization volume under conditions suitable for crystal formation of the protein.

8. (Currently amended) A method according to claim 7 wherein is expressed from a nucleic acid molecule that comprises ~~SEQ. ID No. 2~~ SEQ ID NO:2.

9. (Cancelled)

10. (Currently amended) A method according to claim 7 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution less than 3.0 Angstroms.

11-12.   (Canceled)

13.   (Original) A method according to claim 7, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

14.   (Cancelled)

15.   (Currently amended) A protein ~~composition according~~ to claim 16 where the protein is expressed from a nucleic acid molecule that comprises ~~SEQ. ID No. 2~~ SEQ ID NO:2.

16.   (Currently amended) A ~~composition comprising an isolated~~ a protein consisting of ~~SEQ. ID No. 3~~ residues 13-740 of SEQ ID NO:3.

17.   (Previously presented) A method of identifying an entity that associates with a protein, comprising:

taking structure coordinates from diffraction data obtained from a protein crystal formed according to the method of claim 7; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

18.   (Currently amended) A method according to claim 17 wherein the protein from which the protein crystal is formed is expressed from a nucleic acid molecule that comprises ~~SEQ. ID No. 2~~ SEQ ID NO:2.

19.   (Canceled)

20.   (Original) A method according to claim 17, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

21.   (Original) A method according to claim 17, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

U.S. Serial No.: 10/659,055
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22-23. (Cancelled)

24.　　(New) A protein consisting of residues 39-766 of SEQ ID NO:1.

25.　　(New) A composition comprising a protein in crystalline form, wherein the protein consists of residues of 39-766 of SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a $P2_1$ space group and unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å, $\alpha=\gamma=90°$, $\beta=114.6°$.

26.　　(New) A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising a precipitant solution and a protein that consists of residues 39-766 of SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a $P2_1$ space group and unit cell dimensions, +/- 5%, of a=121.53Å b=124.11Å and c=144.42Å, $\alpha=\gamma=90°$, $\beta=114.6°$; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.